Physiolibrary 3.0

www.physiolibrary.org

Connectors



= Modelica.Fluid.Interfaces.FluidPort

ThermalPort

= Modelica.Thermal.HeatTransfer.Interfaces.HeatPort

Chemical.Interfaces.SubstancePort

= Chemical.Interfaces.SubstancePort

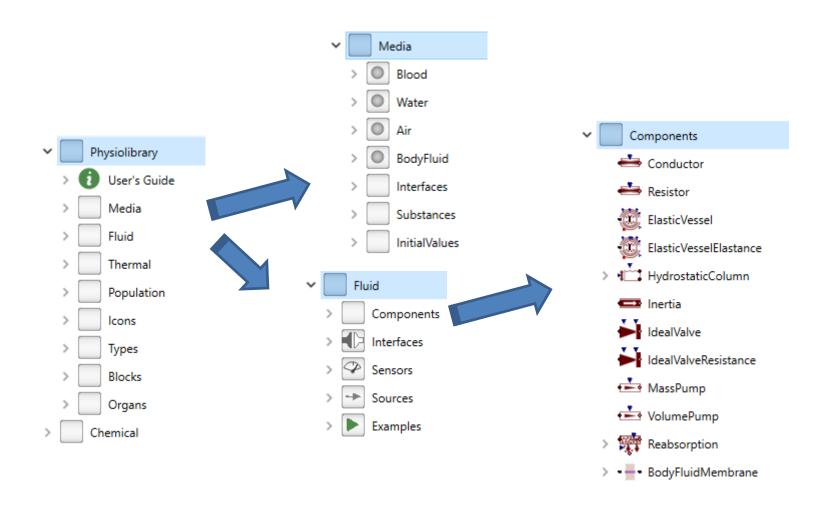
Medium.SubstancesPort

 bundle of electrochemical ports for free base medium substances

PopulationPort

size of population, change of population

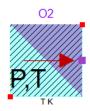
Physiolibrary Structure



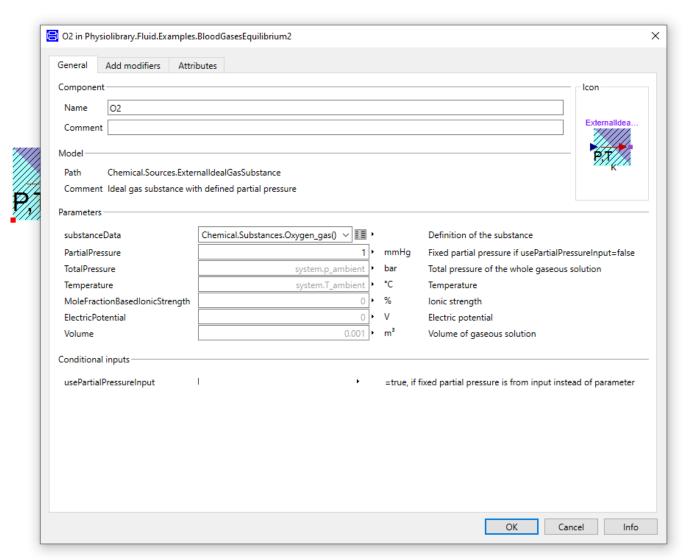
Experiment – blood (de)oxygenation

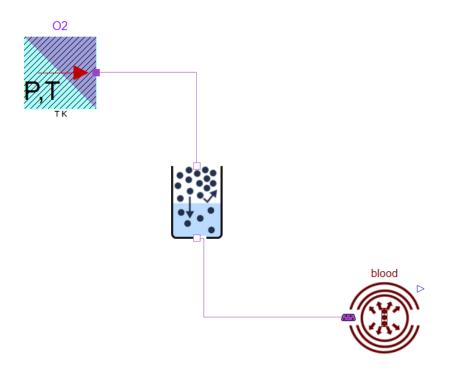


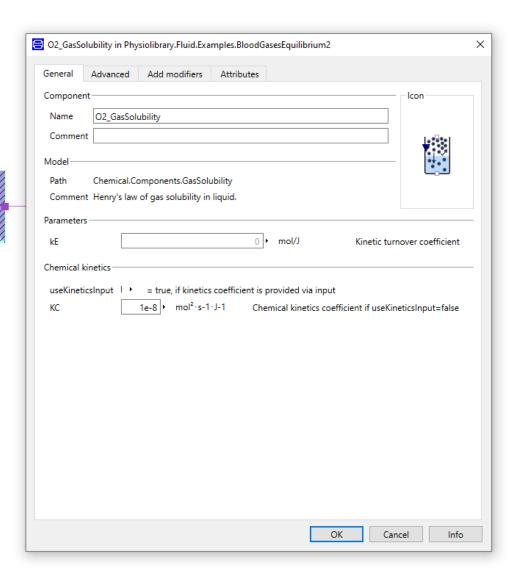
omponent				lcon
Name blood				
Comment				
odel —				- W
	id.Components.ElasticVessel			Page 10 / 10 / 10 / 10 / 10 / 10 / 10 / 10
	nent as chemical solution envelop)		
arameters —				
/ledium		Blood ✓ III ▶		Medium model
nElectricGround				=true, if electric potencial is zero
Compliance		1	ml/mmHg	Compliance e.g. TidalVolume/TidalPressureGradient if
•			illi/illilling	useComplianceInput=false Functional Residual Capacity. Maximal fluid volume, that does not generate
Zero Pressure Volume		1e-05	ml	pressure if useV0Input=false
xternalPressure	if icEvtarnalDraccureAbcolute th	en system.p_ambien	mmHg	External pressure if useExternalPressureInput=false.
	II ISEXTERNAL PRESSURE ADSOLUTE UP			External pressure in ascexternal ressurempate-talse.
,		I F 1	of all base mole to sum==1.	ecules. If size is nS-1 then last value is 1-sum(others). If size is nS then all values
nassFractions_start xtraConcentration_start	position	are scaled	to sum==1.	
nassFractions_start extraConcentration_start	positionBlood.ArterialDefault	are scaled	to sum==1.	per kilogram of solution
nassFractions_start extraConcentration_start tialization emperature_start	positionBlood.ArterialDefault	are scaled	to sum==1.	ecules. If size is nS-1 then last value is 1-sum(others). If size is nS then all values per kilogram of solution system.T_ambient
tialization of medium com nassFractions_start extraConcentration_start tialization emperature_start se_mass_start olume_start	position Blood.ArterialDefault Medium.C_default	are scaled	to sum==1.	ecules. If size is nS-1 then last value is 1-sum(others). If size is nS then all values per kilogram of solution system.T_ambient
nassFractions_start extraConcentration_start itialization emperature_start use_mass_start	position Blood.ArterialDefault Medium.C_default	are scaled	to sum==1.	per kilogram of solution system.T_ambient C Initial temperature Use mass_start, otherwise volume_start
nassFractions_start extraConcentration_start itialization emperature_start use_mass_start olume_start	position Blood.ArterialDefault Medium.C_default	are scaled	to sum==1.	per kilogram of solution system.T_ambient C Initial temperature Use mass_start, otherwise volume_start
nassFractions_start extraConcentration_start tialization emperature_start sse_mass_start olume_start nass_start	position Blood.ArterialDefault Medium.C_default	are scaled	to sum==1.	per kilogram of solution system.T_ambient C Initial temperature Use mass_start, otherwise volume_start
nassFractions_start xtraConcentration_start tialization emperature_start se_mass_start olume_start nass_start onditional inputs seSubstances	position Blood.ArterialDefault Medium.C_default	are scaled	to sum==1.	per kilogram of solution system.T_ambient C Initial temperature Use mass_start, otherwise volume_start 1000 ml Total volume of solution start value Total mass of solution start value
nassFractions_start xtraConcentration_start tialization emperature_start se_mass_start olume_start nass_start onditional inputs seSubstances seThermalPort	position Blood.ArterialDefault Medium.C_default	are scaled	to sum==1.	per kilogram of solution system.T_ambient C Initial temperature Use mass_start, otherwise volume_start 1000 ml Total volume of solution start value Total mass of solution start value =true, if substance ports are used
nassFractions_start xtraConcentration_start tialization emperature_start se_mass_start olume_start nass_start onditional inputs seSubstances seThermalPort	position Blood.ArterialDefault Medium.C_default	are scaled	to sum==1.	per kilogram of solution system.T_ambient C Initial temperature Use mass_start, otherwise volume_start 1000 ml Total volume of solution start value Total mass of solution start value =true, if substance ports are used Is thermal port pressent?
nassFractions_start xtraConcentration_start tialization emperature_start se_mass_start olume_start nass_start onditional inputs seSubstances seThermalPort seV0Input seComplianceInput	position Blood.ArterialDefault Medium.C_default	are scaled	to sum==1.	per kilogram of solution system.T_ambient C Initial temperature Use mass_start, otherwise volume_start 1000 ml Total volume of solution start value Total mass of solution start value start value temperature Use mass_start, otherwise volume_start 1000 ml Total volume of solution start value Total mass of solution start value start value temperature Use mass_start, otherwise volume_start 1000 Is thermal port pressent? start value is used
nassFractions_start xtraConcentration_start tialization emperature_start se_mass_start olume_start nass_start enditional inputs seSubstances seThermalPort seVOInput seComplianceInput seExternalPressureInput	position Blood.ArterialDefault Medium.C_default	are scaled	to sum==1.	per kilogram of solution system.T_ambient C Initial temperature Use mass_start, otherwise volume_start 1000 ml Total volume of solution start value Total mass of solution start value Total mass of solution start value Is thermal port pressent? =true, if zero-pressure-fluid_volume input is used =true, if compliance input is used =true, if external pressure input is used
nassFractions_start extraConcentration_start itialization emperature_start use_mass_start olume_start nass_start	position Blood.ArterialDefault Medium.C_default	are scaled	to sum==1.	per kilogram of solution system.T_ambient C Initial temperature Use mass_start, otherwise volume_start 1000 ml Total volume of solution start value Total mass of solution start value Total mass of solution start value is thermal port pressent? true, if zero-pressure-fluid_volume input is used true, if compliance input is used true, if external pressure input is used

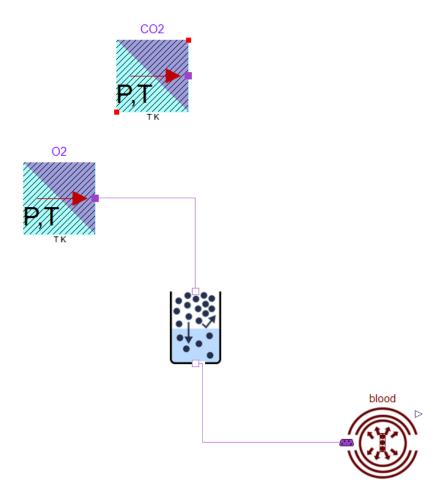


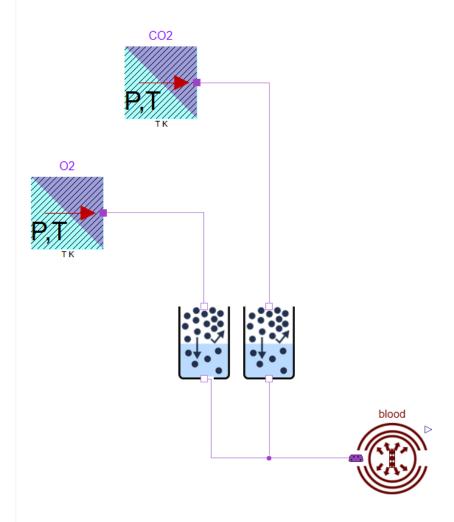


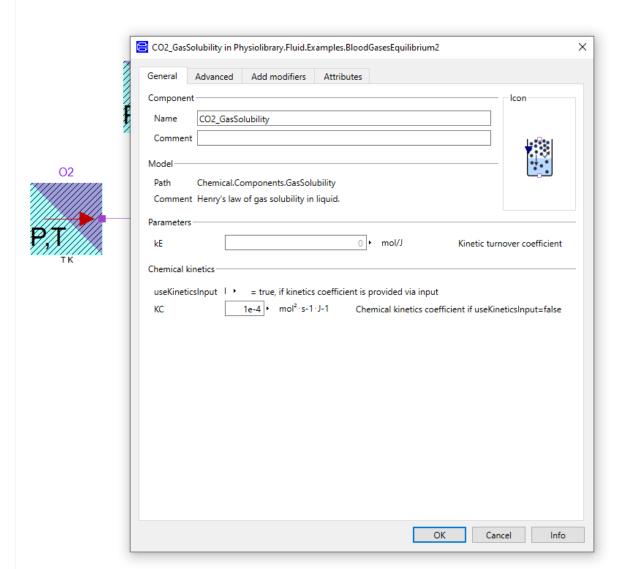


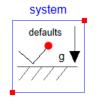




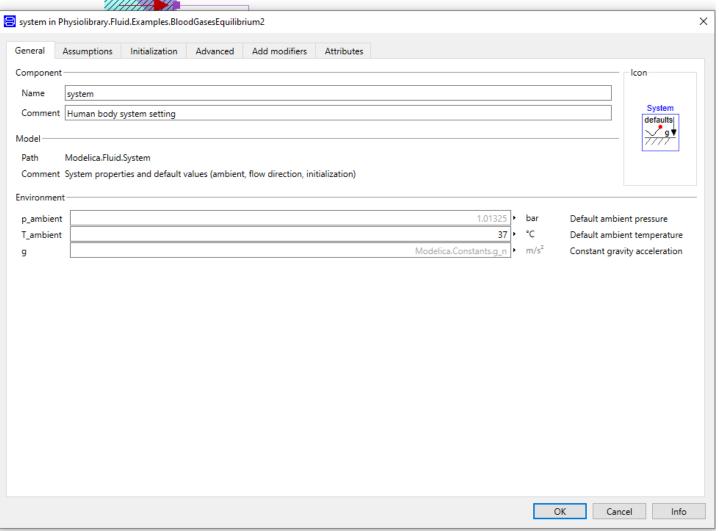








CO2

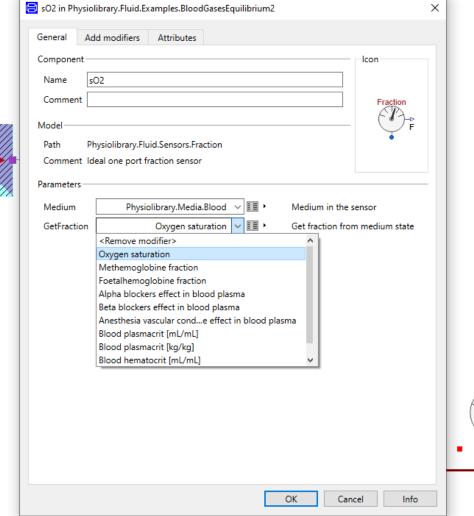


CO2 02 blood s02

system defaults



CO2

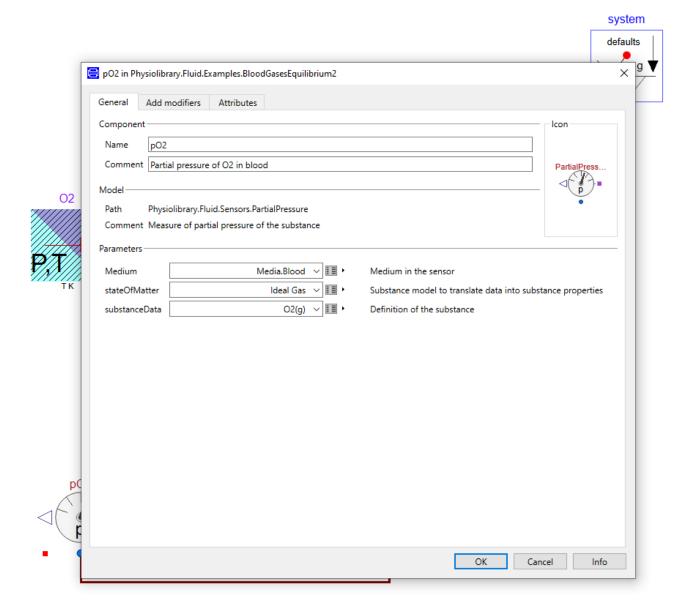




sO2 F

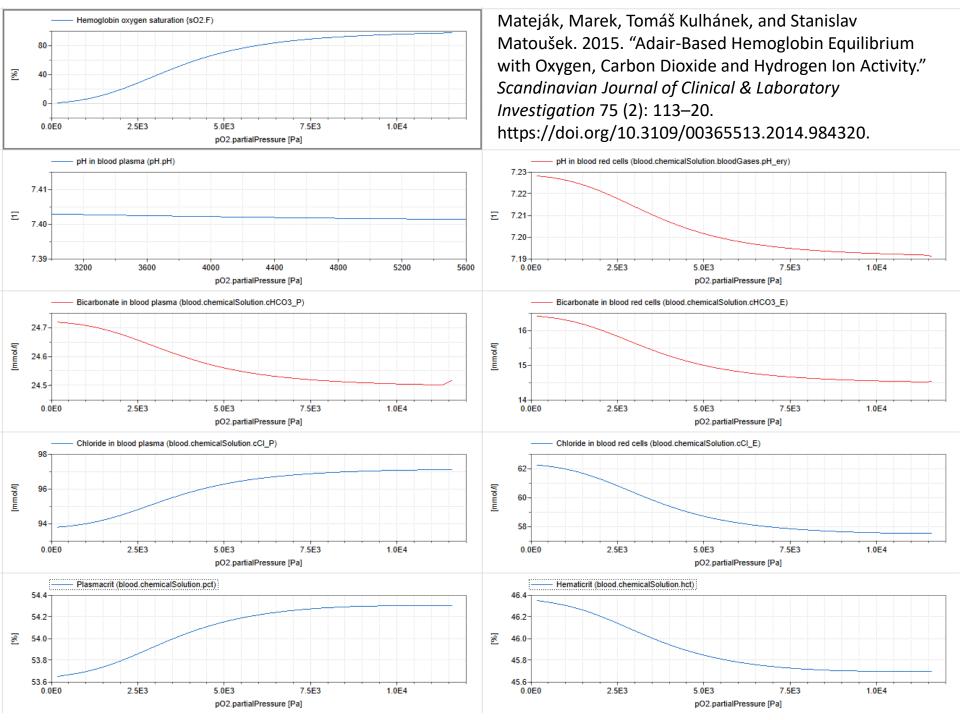
defaults CO2 02 blood sO2 pO2

system

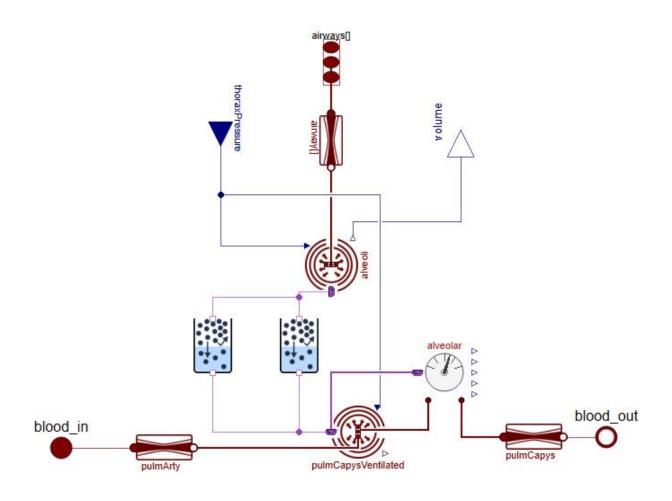


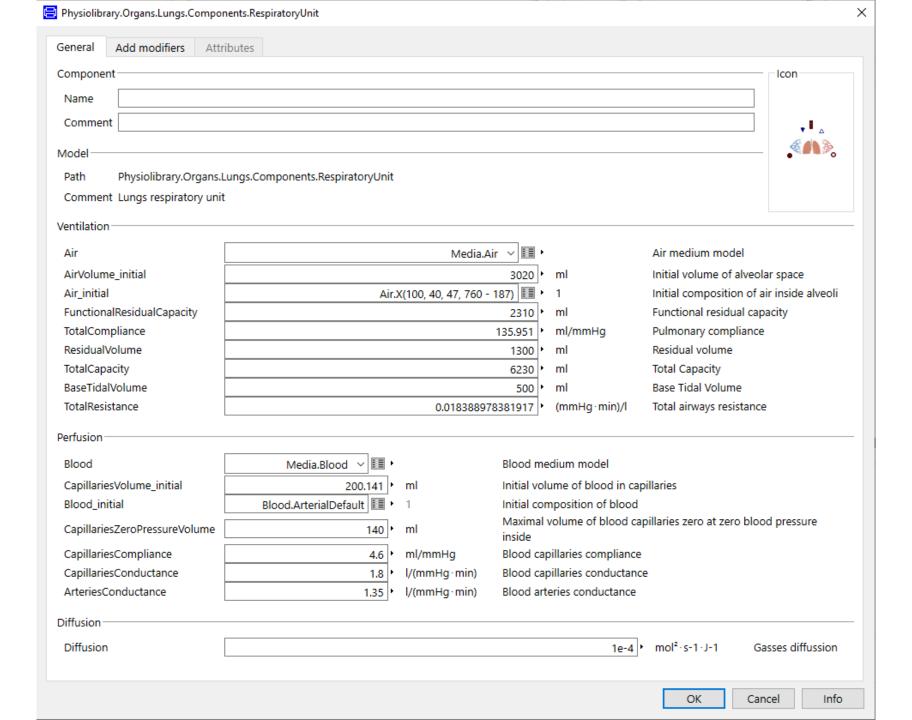
Behind

- Hemoglobin O2, CO2, H+, CO binding
- Henderson-Hasselbalch: CO2 + H2O <-> HCO3- + H+
- Chloride shift: Cl-, HCO3-
- Electroneutrality
- Acid-base
- Osmosis

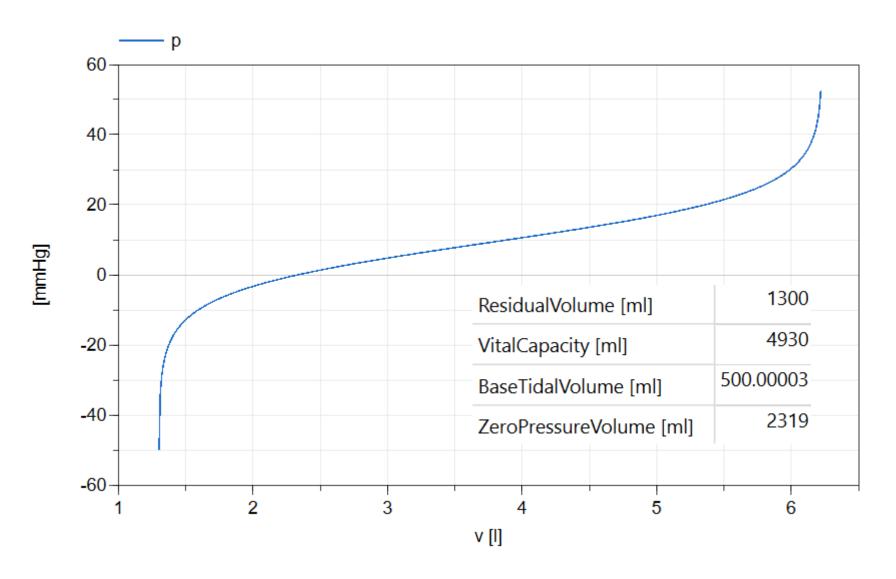


Respiratory unit

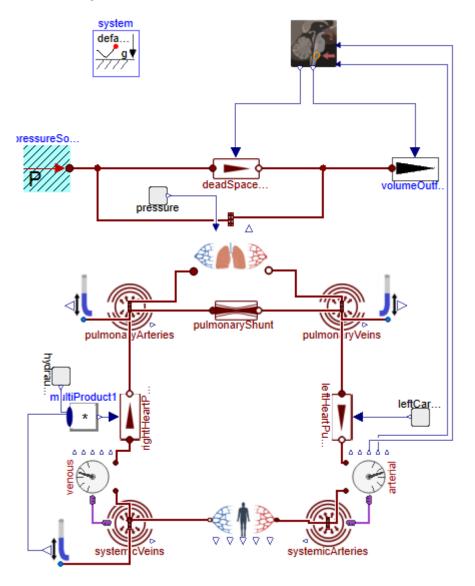


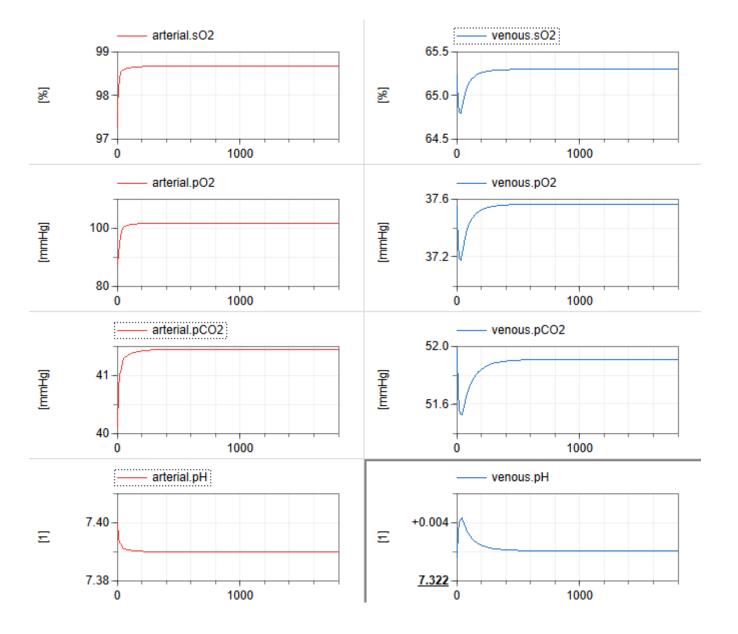


Lungs pressure-volume relation



Mean respiration and circulation





Blood medium

```
extends Media.Interfaces.PartialMedium(
 mediumName = "Blood",
 substanceNames={"H2O P","H2O E","O2","CO2 P","CO2 E","CO","eHb","MetHb","HbF","Alb","Glb","PO4","DPG",
    "Glucose", "Lactate", "Urea", "AminoAcids", "Lipids", "KetoAcids",
   "Na P", "K P", "Na E", "K E", "Cl P", "Cl E",
   "Epinephrine", "Norepinephrine", "Vasopressin",
   "Insulin", "Glucagon", "Thyrotropin", "Thyroxine", "Leptin",
   "Desalvmidodrine",
   "Angiotensin2", "Renin", "Aldosterone",
   "Other P", "Other E"},
 extraPropertiesNames={
                                               redeclare replaceable record extends ThermodynamicState
   "AlphaBlockers",
                                                 "A selection of variables that uniquely defines the thermodynamic state"
   "BetaBlockers",
                                                 extends Modelica. Tcons. Record:
   "AnesthesiaVascularConductance" },
                                                 AbsolutePressure p "Absolute pressure of medium";
                                                 SpecificEnthalpy h "Specific enthalpy";
                                                 MassFraction X[nS] "Mass fractions of substances";
                                                 Types.ElectricPotential v "Electric potential";
                                               end ThermodynamicState;
redeclare connector extends SubstancesPort "Blood chemical substances interface"
     Chemical.Interfaces.SubstancePort a CO2 "Free carbon dioxide molecule";
     Chemical.Interfaces.SubstancePort a 02 "Free oxygen molecule";
     Chemical.Interfaces.SubstancePort a CO "Free carbon monoxide moelcule";
     Chemical.Interfaces.SubstancePort a HCO3 "Free bicarbonate molecule";
     Chemical.Interfaces.SubstancePort a H "Free protons";
     Chemical. Interfaces. SubstancePort a H2O "Free water molecule (in pure water is only cca 1 mol/kg free
     Chemical. Interfaces. SubstancePort a Glucose, Lactate, Urea, AminoAcids, Lipids, KetoAcids;
     Chemical.Interfaces.SubstancePort a Epinephrine, Norepinephrine, Vasopressin;
     Chemical. Interfaces. SubstancePort a Insulin, Glucagon, Thyrotropin, Thyroxine, Leptin;
     Chemical.Interfaces.SubstancePort a Desglymidodrine;
     Chemical.Interfaces.SubstancePort a Angiotensin2, Renin, Aldosterone;
```

end SubstancesPort;

SubstancesPort

```
equation
 connect(02.port a, Artys.substances.02) 3;
 connect(CO2.port a, Artys.substances.CO2) ∃;
 connect(CO.port a, Artys.substances.CO) = ;
 connect(H2O.port a, Artys.substances.H2O) = ;
 connect (H2O.port b, Veins.substances.H2O) ∃;
 connect(Glucose.port a, Artys.substances.Glucose) = ;
 connect(Glucose.port b, Veins.substances.Glucose) ];
 connect(Lactate.port a, Artys.substances.Lactate) = ;
 connect (Lactate.port b, Veins.substances.Lactate) ∃ ;
 connect(Urea.port a, Artys.substances.Urea) = ;
 connect(Urea.port b, Veins.substances.Urea) 3;
 connect(AminoAcids.port a, Artys.substances.AminoAcids) a;
 connect(AminoAcids.port b, Veins.substances.AminoAcids) = ;
 connect(Hormones[1].port a, Artys.substances.Epinephrine) 3;
 connect(Hormones[2].port a, Artys.substances.Norepinephrine) = ;
 connect(Hormones[2].port b, Veins.substances.Norepinephrine) = ;
```

ArterialDefault

Venous Default

Blood - setting

CDefault

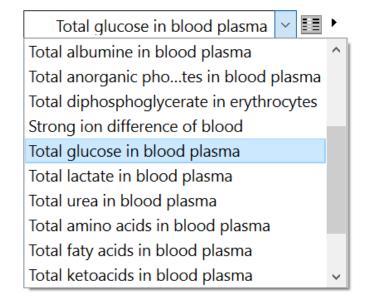
ArterialComposition

VenousComposition

```
package InitialValues
 import Physiolibrary.Media.Substances.*;
 constant Types.Density D BloodDensity=1057 "Density of blood";
 constant Types.Density D BloodPlasmaDensity=1025 "Density of blood plasma";
 constant Types. VolumeFraction D Hct = 0.44 "Default hematocrit [ml/ml]";
 constant Types.Concentration
       D Na = 138.5 "Default sodium in blood plasma",
       D K = 4 "Default potassium in blood plasma",
       D Cl = 103 "Default chloride in blood plasma",
       D Na RBC = 7 "Default sodium in blood red cells",
       D K RBC = 96 "Default potassium in blood red cells",
       D Cl RBC = 50 "Default chloride in blood red cells";
 constant Real D SID P = D Na+D K-D Cl;
 constant Real D SID RBC = D Na RBC+D K RBC-D Cl RBC;
 constant Types.Concentration
       D Glucose = 6.08 "Default glucose in blood plasma",
       D Lactate = 1.04 "Default lactate in blood plasma",
       D Urea = 6.64 "Default urea in blood plasma",
       D AminoAcids = 4.97 "Default amino acids in blood plasma",
      D Lipids = 1.23 "Default lipids in blood plasma",
       D Ketoacids = 4.88e-2 "Default keto acids in blood plasma";
 constant Types.Concentration D Arterial O2 = 8.16865 "Default Total oxygenin arterial blood",
```

Blood - output

```
function glucose "Total glucose in blood plasma"
                                                                                replaceable function GetConcentration =
                                                                                    Physiolibrary.Media.Blood.t02
  extends GetConcentration;
                                                                                  constrainedby
algorithm
                                                                                    Medium.GetConcentration
  C := (plasmaDensity(state) *state.X[i("Glucose")]/Constants.MM Glucose)/
                                                                                  "Get concentration from medium state"
    plasmaMassFraction(state);
                                                                                    annotation (choicesAllMatching=true);
end glucose;
                                                                                replaceable function GetFraction =
                                                                                    Physiolibrary.Media.Blood.hematocrit
function sO2 "Oxygen saturation on effective hemoglobin"
                                                                                  constrainedby Medium.GetFraction
 extends GetFraction;
algorithm
                                                                                  "Get fraction from medium state"
 F := (state.X[i("02")] / 02.MolarWeight) / (state.X[i("eHb")] / Constants.MM Hb);
                                                                                    a ;
end sO2;
```



Oxygen saturation on effective her Image: Text of the content of the

Thank you for your attention!